WATER RESOURCES RESEARCH GRANT PROPOSAL

Project ID: 2005PA41B

Title: Fatty acid methyl ester (FAME) profiles of Escherichia coli and enterococci for predicting sources of microbial pollution

Project Type: Research

Focus Categories: Water Quality, Surface Water, Non Point Pollution

Keywords: microbial contamination, fecal pollution, indicator organisms, Escherichia coli, enterococci, fatty acid methyl ester (FAME) profiling

Start Date: 03/01/2005

End Date: 02/28/2006

Federal Funds: $17,560

Non-Federal Matching Funds: $39,525

Congressional District: 7th

Principal Investigator:
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Abstract

The overall objective of this study is to investigate the host-specific differences in fatty acid methyl ester (FAME) profiles of Escherichia coli and enterococci for the purpose of predicting sources of microbial pollution in water environments. Effective methods for microbial source tracking (MST) are needed to ensure timely and precise response to protect human and environmental health and to develop more accurate Total Maximum Daily Load (TMDL) programs to maintain long-term water quality.

Microbial contamination is one of the major water quality issues. Pathogens associated with fecal pollution affect many water environments in the US and around the world. The Year 2000 National Water Quality Inventory lists microbial contamination as the leading cause of water quality impairment in rivers and streams in the US (USEPA, 2000). In fact, pathogens are the second leading cause of water quality impairment nationwide (EPA Section 303d List). There are over 1500 water environments on TMDL programs due to the presence of pathogens. Microbial pollution can lead to human diseases and economic losses in industries that depend on coastal water quality, such as shell fisheries.

The proposed study will develop a database of approximately 1,500 isolates of E. coli and enterococci from possible sources of microbial contamination including human, livestock, and wildlife. Then E. coli and enterococci isolates cultured from water environments affected by microbial contamination will be compared to the known-host library for predicting their host origins.

It is expected that this new technology will provide a reliable, economical, and effective means of sources identification for microbial pollution and thus contribute significantly to source water protection efforts. This new technology will enable all water resources organizations even the ones with limited budget, such as small grass-root organizations and township officials, to monitor presence and sources of pathogens routinely. In addition, the project will provide training opportunity for students and water quality professionals.